

94

Gln: R, Arg; S, Ser; T, Thr; V, Val; W, Trp; and Y, Tyr.] The DNA binding region and hydrophobic repeats delineated by conserved sequence blocks are indicated by the filled and diagonally striped sections, respectively. The shaded section represents the 12-residue element conserved among vertebrate HSFs. The open and filled triangles denote hydrophobic residues at positions (a) and (d) of the heptad repeat. The gel mobility-shift analysis on extracts from unshocked (37°C) and heat-shocked (44°C) transfected cells shown at right was carried out as described (17) [17. S.K. Rabindran, G. Giorgi, J. Clos. C. Wu, Proc. Natl. Acad. Sci. U.S.A. 88, 6906 (1991)]. Swith a <sup>32</sup>P-labeled consensus HSE containing three [nGAAn] modules. Only the complex of HSF bound to the HSE is shown.

Figure 1 is reproduced as Figure 16.

In the Figures:

~~ME~~ Please add Figures 13-16

In the Claims:

Claim 1, line 3, delete "a", insert --an antibody--

Please cancel claim 2.

Claims 3 and 4, line 1, delete "2", insert --1--

Claim 6, line 7, delete "phosphoylase", insert --  
phosphorylase--

Claim 9, (amended) The nucleic acid delivery system of claim 1, wherein the nucleic acid segment comprises [flanking 5' and 3' long terminal repeat LTR regions or inverted terminal repeat (ITR) regions,] a promoter operably linked to a desired gene in the nucleic acid sequence of interest, wherein said promoter and gene are flanked by 5' and 3' long terminal repeat (LTR) regions or inverted terminal repeat (ITR) regions.

Remarks